

SEQUENCE LISTING

<110> Hastings, Gregg
Dillon, Patrick

<120> Human Neuronal Attachment Factor-1

<130> PF226D1

<140> 09/170,042

<141> 1988-10-13

<160> 19

<170> PatentIn version 3.0

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<212> DNA

<213> homo sapiens

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Lys Ala Leu Cys Ala Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln
15 20 25

cct ctt ggg gga gag tcc atc tgt tcc gcc aga gcc ctg gcc aaa tac 147
Pro Leu Gly Gly Glu Ser Ile Cys Ser Ala Arg Ala Leu Ala Lys Tyr
30 35 40

agc atc acc ttc acg ggc aag tgg agc cag acg gcc ttc ccc aag cag 195
Ser Ile Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln
45 50 55

tac ccc ctg ttc cgc ccc cct gcc cag tgg tct tcg ctg ctg ggg gcc 243
Tyr Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala
60 65 70 75

gcg cat agc tcc gac tac agc atg tgg agg aag aac cag tac gtc agt 291
Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val Ser
80 85 90

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Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala Leu Met
95 100 105

aag gag atc gag gcg gcg ggg gag gcg ctg cag agc gtg cac gcg gtg 387
Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val His Ala Val
110 115 120

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Phe Ser Ala Pro Ala Val Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu
125 130 135

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| ctg gag gtg cag cgc agg cac tcg ctg gtc tcg ttt gtg gtg cgc atc | 483 |
| Leu Glu Val Gln Arg Arg His Ser Leu Val Ser Phe Val Val Arg Ile | |
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| gtg ccc agc ccc gac tgg ttc gtg ggc gtg gac agc ctg gac ctg tgc | 531 |
| Val Pro Ser Pro Asp Trp Phe Val Gly Val Asp Ser Leu Asp Leu Cys | |
| 160 165 170 | |
| gac ggg gac cgt tgg cgg gaa cag gcg gcg ctg gac ctg tac ccc tac | 579 |
| Asp Gly Asp Arg Trp Arg Glu Gln Ala Ala Leu Asp Leu Tyr Pro Tyr | |
| 175 180 185 | |
| gac gcc ggg acg gac agc ggc ttc acc ttc tcc tcc ccc aac ttc gcc | 627 |
| Asp Ala Gly Thr Asp Ser Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala | |
| 190 195 200 | |
| acc atc ccg cag gac acg gtg acc gag ata acg tcc tcc tct ccc agc | 675 |
| Thr Ile Pro Gln Asp Thr Val Thr Glu Ile Thr Ser Ser Pro Ser | |
| 205 210 215 | |
| cac ccg gcc aac tcc ttc tac tac ccg cgg ctg aag gcc ctg cct ccc | 723 |
| His Pro Ala Asn Ser Phe Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro | |
| 220 225 230 235 | |
| atc gcc agg gtg aca ctg gtg cgg ctg cga cag agc ccc agg gcc ttc | 771 |
| Ile Ala Arg Val Thr Leu Val Arg Leu Arg Gln Ser Pro Arg Ala Phe | |
| 240 245 250 | |
| atc cct ccc gcc cca gtc ctg ccc agc agg gac aat gag att gta gac | 819 |
| Ile Pro Pro Ala Pro Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp | |
| 255 260 265 | |
| agc gcc tca gtt cca gaa acg ccg ctg gac tgc gag gtc tcc ctg tgg | 867 |
| Ser Ala Ser Val Pro Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp | |
| 270 275 280 | |
| tcg tcc tgg gga ctg tgc gga ggc cac tgt ggg agg ctc ggg acc aag | 915 |
| Ser Ser Trp Gly Leu Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys | |
| 285 290 295 | |
| agc agg act cgc tac gtc cgg gtc cag ccc gcc aac aac ggg agc ccc | 963 |
| Ser Arg Thr Arg Tyr Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro | |
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| tgc ccc gag ctc gaa gaa gag gct gag tgc gtc cct gat aac tgc gtc | 1011 |
| Cys Pro Glu Leu Glu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys Val | |
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| taagaccaga gccccgcagc ccctggggcc ccccgagacc atgggggtgtc gggggctcct | 1071 |
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 35 40 45
 Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr Pro Leu Phe Arg
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 Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala Ala His Ser Ser Asp
 65 70 75 80
 Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val Ser Asn Gly Leu Arg Asp
 85 90 95
 Phe Ala Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala
 100 105 110
 Ala Gly Glu Ala Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala
 115 120 125
 Val Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val Gln Arg
 130 135 140
 Arg His Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp
 145 150 155 160
 Trp Phe Val Gly Val Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp
 165 170 175
 Arg Glu Gln Ala Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp
 180 185 190
 Ser Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp
 195 200 205
 Thr Val Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser
 210 215 220
 Phe Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr
 225 230 235 240
 Leu Val Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala Pro

245

250

255

Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser Val Pro
 260 265 270

Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu
 275 280 285

Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser Arg Thr Arg Tyr
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Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro Cys Pro Glu Leu Glu
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Glu Glu Ala Glu Cys Val Pro Asp Asn Cys Val
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<222> (1)..(36)

<223> 5' primer containing a BamHI restriction enzyme site followed by
 21 nucleotides of NAD-1 coding sequence.

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<211> 35

<212> DNA

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<223> 3' primer containing complementary sequence to an XbaI site
 followed by 21 nucleotides of NAF-1 sequence.

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35

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<211> 41

<212> DNA

<213> oligonucleotide

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 <223> 5' primer containing a BamHI restriction enzyme site followed by
 8 nucleotides resembling an efficient signal for initiation of
 translation in eukaryotic cells followed by 21 nucleotides of
 NAF-1 sequence.

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 <211> 35
 <212> DNA
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 <221> primer_bind
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 <223> 3' primer containing the cleavage site for XbaI restriction
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 <212> PRT
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<400> 7

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| Pro | Thr | Gly | Thr | Gly | Cys | Val | Ile | Leu | Lys | Ala | Ser | Ile | Val | Gln | Lys | 1 | 5 | 10 | 15 |
| Arg | Ile | Ile | Tyr | Phe | Gln | Asp | Glu | Gly | Ser | Leu | Thr | Lys | Lys | Leu | Cys | 20 | 25 | 30 | |
| Glu | Gln | Asp | Pro | Thr | Leu | Asp | Gly | Val | Thr | Asp | Arg | Pro | Ile | Leu | Asp | 35 | 40 | 45 | |
| Cys | Cys | Ala | Cys | Gly | Thr | Ala | Lys | Tyr | Arg | Leu | Thr | Phe | Tyr | Gly | Asn | 50 | 55 | 60 | |
| Trp | Ser | Glu | Lys | Thr | His | Pro | Lys | Asp | Tyr | Pro | Arg | Arg | Ala | Asn | His | 65 | 70 | 75 | 80 |
| Trp | Ser | Ala | Ile | Ile | Gly | Gly | Ser | His | Ser | Lys | Asn | Tyr | Val | Leu | Trp | 85 | 90 | 95 | |
| Glu | Tyr | Gly | Gly | Tyr | Ala | Ser | Glu | Gly | Val | Lys | Gln | Val | Ala | Glu | Leu | 100 | 105 | 110 | |
| Gly | Ser | Pro | Val | Lys | Met | Glu | Glu | Glu | Ile | Arg | Gln | Gln | Ser | Asp | Glu | 115 | 120 | 125 | |
| Val | Leu | Thr | Val | Ile | Lys | Ala | Lys | Ala | Gln | Trp | Pro | Ser | Trp | Gln | Pro | | | | |

| 130 | 135 | 140 |
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| Val Asn Val Arg Ala Ala Pro Ser Ala Glu Phe Ser Val Asp Arg Thr | | |
| 145 | 150 | 155 160 |
| Arg His Leu Met Ser Phe Leu Thr Met Met Gly Pro Ser Pro Asp Trp | | |
| | 165 | 170 175 |
| Asn Val Gly Leu Ser Ala Glu Asp Leu Cys Thr Lys Glu Cys Gly Trp | | |
| | 180 | 185 190 |
| Val Gln Lys Val Val Gln Asp Leu Ile Pro Trp Asp Ala Gly Thr Asp | | |
| | 195 | 200 205 |
| Ser Gly Val Thr Tyr Glu Ser Pro Asn Lys Pro Thr Ile Pro Gln Glu | | |
| | 210 | 215 220 |
| Lys Ile Arg Pro Leu Thr Ser Leu Asp His Pro Gln Ser Pro Phe Tyr | | |
| | 225 | 230 235 240 |
| Asp Pro Glu Gly Gly Ser Ile Thr Gln Val Ala Arg Val Val Ile Glu | | |
| | 245 | 250 255 |
| Arg Ile Ala Arg Lys Gly Glu Gln Cys Asn Ile Val Pro Asp Asn Val | | |
| | 260 | 265 270 |
| Asp Asp Ile Val Ala Asp Leu Ala Pro Glu Glu Lys Asp Glu Asp Asp | | |
| | 275 | 280 285 |
| Thr Pro Glu Thr Cys Ile Tyr Ser Asn Trp Ser Pro Trp Ser Ala Cys | | |
| | 290 | 295 300 |
| Ser Ser Ser Thr Cys Glu Lys Gly Lys Arg Met Arg Gln Arg Met Leu | | |
| | 305 | 310 315 320 |
| Lys Ala Gln Leu Asp Leu Ser Val Pro Cys Pro Asp Thr Gln Asp Phe | | |
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| Gln Pro Cys Met Gly Pro Gly Cys Ser Asp Glu Asp Gly Ser Thr Cys | | |
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| Thr Met Ser Glu Trp Ile Thr Trp Ser Pro Cys Ser Val Ser Cys Gly | | |
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| | 370 | 375 380 |
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| Gly Pro Gly Cys | | |
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| Gly Met Gly Met Arg Ser Arg Glu Arg Tyr Val Lys Gln Phe Pro Glu | | |
| 20 | 25 | 30 |
| Asp Gly Ser Val Cys Met Leu Pro Thr Glu Glu Thr Glu Lys Cys Thr | | |
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| Val Asn Glu Glu Cys | | |
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| 35 | 40 | 45 |
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| 1 | 5 | 10 15 |
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Phe Gly Gly Ala Pro Cys Pro Glu Thr Val Gln Arg Lys Lys Cys Arg
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Ala Arg Lys Cys
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Gly Gly Gly Ile Gln Glu Arg Tyr Met Thr Val Lys Lys Arg Phe Lys
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Ser Ser Gln Phe Thr Ser Cys Lys Asp Lys Lys Glu Ile Arg Ala Cys
35 40 45

Asn Val His Pro Cys
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Gly Ser Pro Cys Pro Asp Thr Glu Glu Ala Glu Lys Cys Met Val Pro
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Glu Cys
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 cagagccccg gccaaataca gcatcacctt cacgggcaag tggagccaga cggccttccc 180
 caagcagtac cccctgttcc gccccctgc gcatggtnnt cgctgctggg ggccgcgcat 240
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 ncggagcggc gaggcctnng ncgttgatga aggagatccg ggnggcgggg gaggcgtnc 360
 anaggtgnca agagttnttt tcggggcccg gttccccaan ggnaacnggn aaacgttggg 420
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| cgccccggtnn cccagcgnca ccnggcagac gtcggcgaac tggtaggtgc agcgcaggca | 180 |
| ctcgctggtc tcgtttgtgg tgcgcacgt gccagcccc gactgggtcg tgggcgtgga | 240 |
| cagcctggga cctgtganaa cggggacctt tngcgnana cagcgncgt tggacctgta | 300 |
| nccctacgac gncggg | 316 |

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cgccccggttn cccagcgnca ccnggcagac gtcggcgaac tgg naggtgc agcgcaggca 180
ctcgctggtc tcgtttgtgg tgcgcacgt gccagcccc gactggttcg tgggcgtgga 240
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| Cys | Glu | Val | Ser | Leu | Trp | Ser | Ser | Trp | Gly | Leu | Cys | Gly | Gly | His | Cys |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Arg | Leu | Gly | Thr | Lys | Ser | Arg | Thr | Arg | Tyr | Val | Arg | Val | Gln | Pro |
| | | | 20 | | | | | 25 | | | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Asn | Gly | Ser | Pro | Cys | Pro | Glu | Leu | Glu | Glu | Glu | Ala | Glu | Cys |
| | | 35 | | | | | 40 | | | | | | 45 | | |

| | | | | |
|-----|-----|-----|-----|-----|
| Val | Pro | Asp | Asn | Cys |
| | 50 | | | |